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1007411-55273860

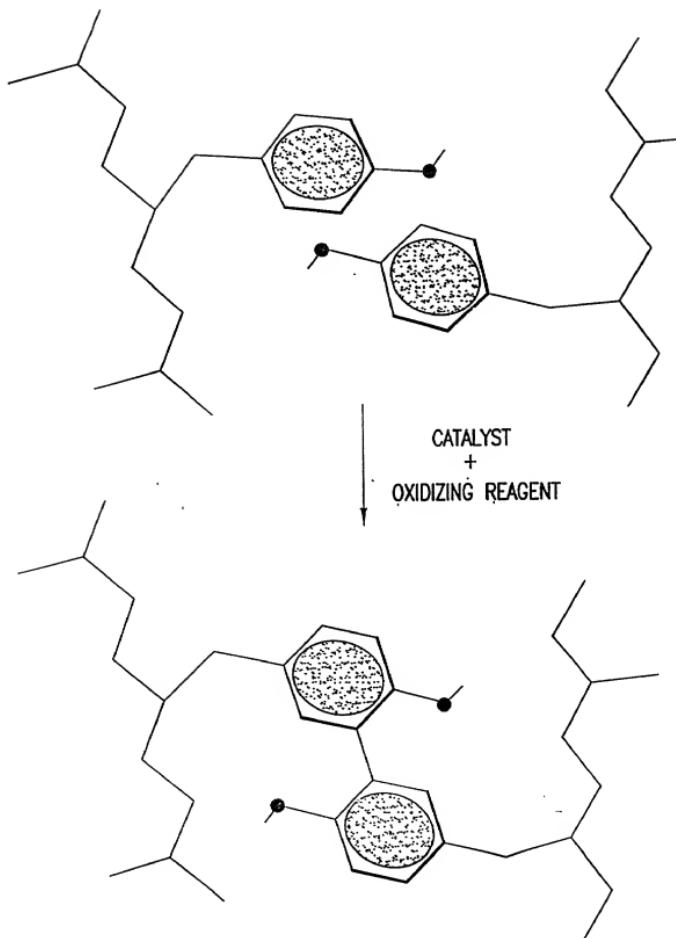


FIG.1A

TODAY'S DATE: 5/22/2000

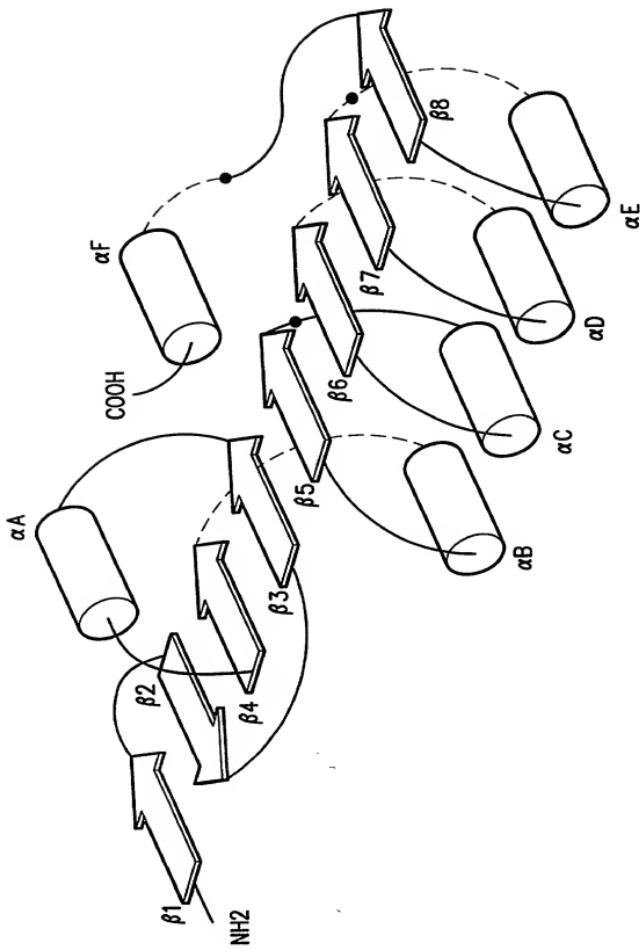


FIG.1B

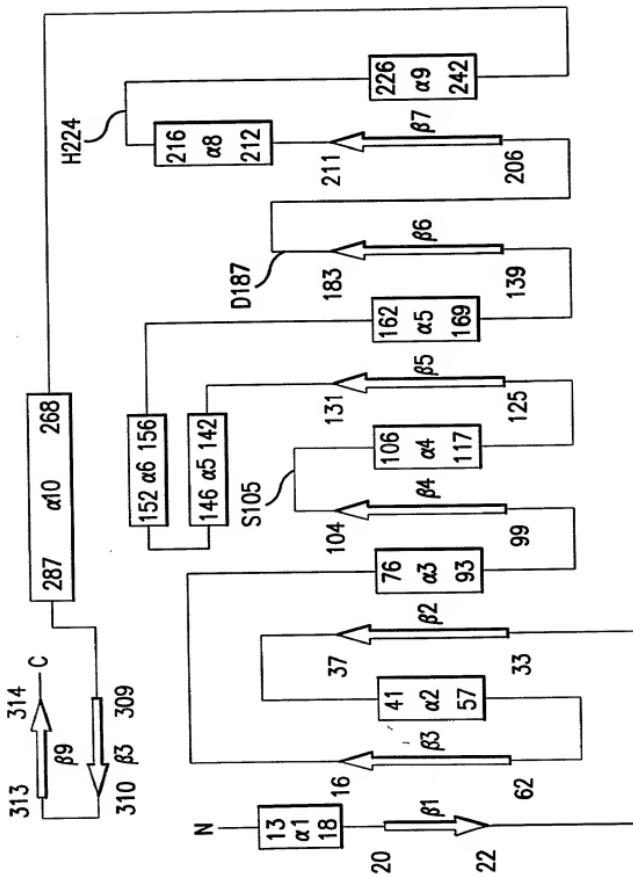


FIG.1C

TOP SECRET//SECURITY

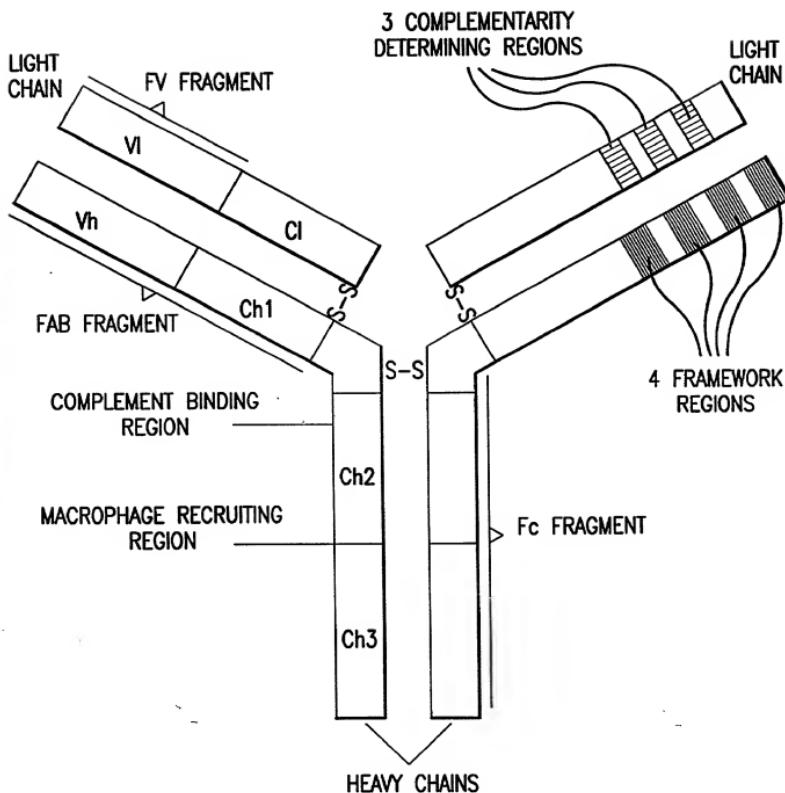


FIG.1D

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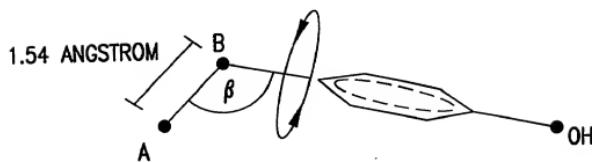


FIG.2A

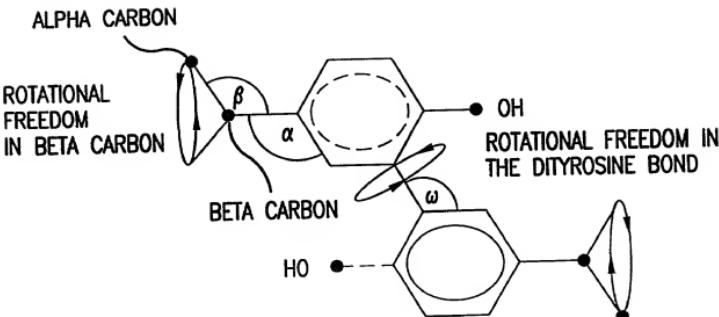


FIG.2B

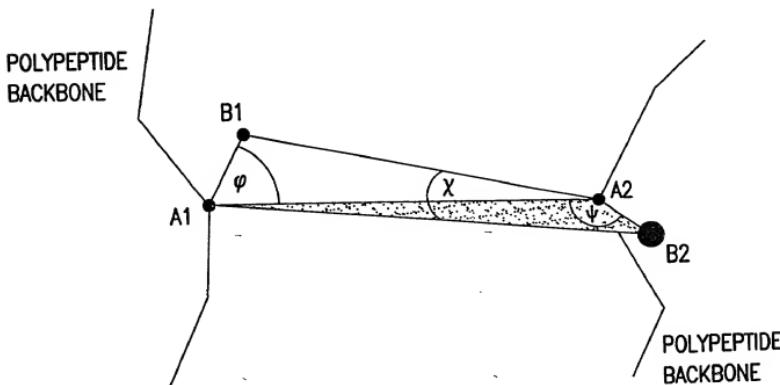


FIG.2C

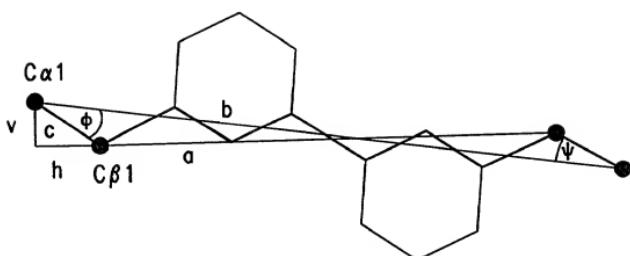


FIG.3A

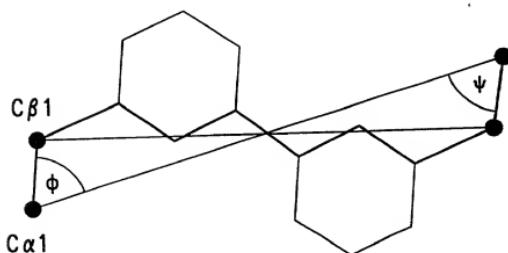


FIG.3B

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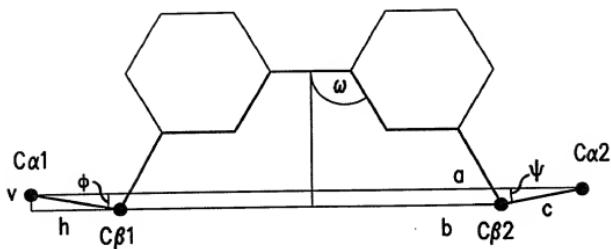


FIG.4A

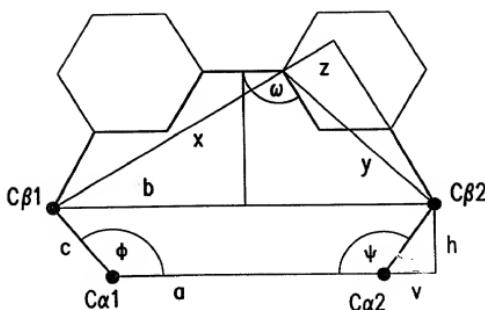


FIG.4B

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LIGHT CHAIN (L)

CHAIN	K&W	ATOM	AMINO ACID	x COORDINATE	y COORDINATE	z COORDINATE
L	1	N	ASP	2.37	-5.00	-27.24
L	1	C α	ASP	2.98	-3.78	-26.64
L	1	C	ASP	1.91	-2.70	-26.52
L	1	O	ASP	1.33	-2.29	-27.53
L	1	C β	ASP	4.14	-3.29	-27.53
L	1	C γ	ASP	5.18	-2.49	-26.76
L	1	O $\delta 1$	ASP	4.86	-1.38	-26.27
L	1	O $\delta 2$	ASP	6.34	-2.97	-26.65
L	2	N	ILE	1.63	-2.26	-25.30
L	2	C α	ILE	0.60	-1.24	-25.07
L	2	C	ILE	1.19	0.15	-24.94
L	2	O	ILE	2.14	0.35	-24.94
L	2	C β	ILE	-0.21	-1.52	-23.78
L	2	C $\gamma 1$	ILE	-0.90	-2.88	-23.86
L	2	C $\gamma 2$	ILE	-1.24	-0.43	-23.58
L	2	C $\delta 1$	ILE	-1.66	-3.26	-22.59
L	3
.
.

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FIG. 5A

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HEAVY CHAIN (H)

CHAIN	K&W	ATOM	AMINO ACID	x COORDINATE	y COORDINATE	z COORDINATE
H	1	N	GLU	11.12	-2.19	9.00
H	1	C α	GLU	11.43	-1.08	8.05
H	1	C	GLU	11.93	-1.63	6.71
H	1	O	GLU	13.10	-1.98	6.56
H	1	C β	GLU	12.47	-0.12	8.66
H	1	C γ	GLU	13.82	-0.75	9.05
H	1	C δ	GLU	13.70	-1.77	10.17
H	1	O $\epsilon 1$	GLU	13.38	-1.36	11.31
H	1	O $\epsilon 2$	GLU	13.94	-2.97	9.92
H	2	N	ILE	11.02	-1.70	5.74
H	2	C α	ILE	11.36	-2.24	4.42
H	2	C	ILE	12.10	-1.22	3.59
H	2	O	ILE	11.77	-0.04	3.64
H	2	C β	ILE	10.11	-2.68	3.62
H	2	C $\gamma 1$	ILE	9.31	-3.73	4.39
H	2	C $\gamma 2$	ILE	10.52	-3.22	2.28
H	3	C $\delta 1$	ILE	8.49	-3.17	5.55
H	3
.
.

FIG.5B

09837235, 04-14-2021

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Fv FRAGMENT 1

Ch	L	L	L	L	L
K&W	1	2	3	4	5
At	C α				
AA	Asp	Ile	.	.	.
x	2.98	0.60	.	.	.
y	-3.78	-1.24	.	.	.
z	-26.64	-25.07	.	.	.

Ch	K&W	At	AA	x	y	z			
H	1	C α	Glu	11.43	-1.08	8.05	35.80	34.84	.
H	2	C α	Ile	11.36	-2.24	4.42	32.21	31.42	.
H	3	C α
H	4	C α
H	5	C α

FIG.6A

Fv FRAGMENT 2

Ch	L	L	L	L	L
K&W	1	2	3	4	5
At	C α				
AA	Glu	Ser	.	.	.
x	35.61	31.94	.	.	.
y	83.10	83.89	.	.	.
z	56.99	56.85	.	.	.

Ch	K&W	At	AA	x	y	z			
H	1	C α	Glu	10.23	61.09	64.74	34.48	32.46	.
H	2	C α	Val	13.63	62.72	65.19	31.07	29.20	.
H	3	C α
H	4	C α
H	5	C α

FIG.6B

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Fv FRAGMENT 3

Ch	Ch					L				
K&W	1	2	3	4	5	C α				
At						Glu	Ser	.	.	.
AA						19.56	19.09	.	.	.
x						-13.02	-15.06	.	.	.
y						-15.86	-12.67	.	.	.
z										

Ch	K&W	At	AA	x	y	z				
H	1	C α	GLN	26.71	9.76	10.88				
H	2	C α	Val	27.45	8.61	7.34				
H	3	C α				
H	4	C α				
H	5	C α				

FIG.6C

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RESIDUE PAIRS		AVERAGE	ST.DEV.	MAX	MIN	MEDIAN
H1	L1	35.38	0.78	35.84	34.48	35.80
H1	L2	34.12	1.44	35.05	32.46	34.84
H1	L3
H1	L4
.
H1	L106
H2	L1	31.99	0.83	32.69	31.07	32.21
H2	L2	30.91	1.52	32.11	29.20	31.41
H2	L3
H2	L4
.
H2	L106
H3	L1

FIG.7A

RESIDUE PAIRS		AVERAGE	ST.DEV.	MAX	MIN	MEDIAN
H1	L1	35.09	1.56	37.37	31.23	35.54
H1	L2	34.00	1.87	37.36	29.92	34.38
H1	L3
H1	L4
.
H1	L106
H2	L1	32.26	1.57	36.71	30.34	32.14
H2	L2	31.32	1.99	36.77	29.20	31.11
H2	L3
H2	L4
.
H2	L106
H3	L1

FIG.7B

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Ch	L	L	L	L	L
K&W	1	2	3	4	5
At	$C\beta$	$C\beta$	$C\beta$	$C\beta$	$C\beta$
AA	ASP	ILE	.	.	.
x	4.14	-0.21	.	.	.
y	-3.29	-1.52	.	.	.
z	-27.53	-23.78	.	.	.

Ch	K&W	At	AA	x	y	z			
H	1	$C\beta$	GLU	12.47	-0.12	8.66	37.27	34.85	.
H	2	$C\beta$	ILE	10.11	-2.68	3.62	31.73	29.30	.
H	3	$C\beta$
H	4	$C\beta$
H	5	$C\beta$

FIG.8

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ALPHA DISTANCES							Ch	L	L	L	L	L	L
Ch	K&W	At	AA	x	y	z	K&W	1	2	3	4	5	
H	1	C α	GLU	11.43	-1.08	8.05	At	C α					
H	2	C α	ILE	11.36	-2.24	4.42	AA	ASP	ILE	.	.	.	
H	3	C α	x	2.98	0.60	.	.	.	
H	4	C α	y	-3.78	-1.24	.	.	.	
H	5	C α	z	-26.64	-25.07	.	.	.	

FIG.9A

BETA DISTANCES							Ch	L	L	L	L	L	L
Ch	K&W	At	AA	x	y	z	K&W	1	2	3	4	5	
H	1	C β	GLU	12.47	-0.12	8.66	At	C β					
H	2	C β	ILE	10.11	-2.68	3.62	AA	ASP	ILE	.	.	.	
H	3	- C β	x	4.14	-0.21	.	.	.	
H	4	C β	y	-3.29	-1.52	.	.	.	
H	5	C β	z	-27.53	-23.78	.	.	.	

FIG.9B

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09837235 004.1601

DIFFERENCE			Ch	L	L	L	L	L
			K&W	1	2	3	4	5
DIFFERENCES BETWEEN RESIDUE PAIR			AA	ASP	ILE	.	.	.
H	1	GLU						
H	2	ILE						
H	3
H	4
H	5

-1.47 -0.01 . . .
0.48 2.10 . . .

FIG.9C

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TOP SECRET//NOFORN//REF ID: A6512965

		L1	L2	L3	L4	L5	.	.
Fv FRAGMENT 1	H1	-1.47	-0.01
	H2	0.48	2.10
	H3
	H4

	.	L1	L2	L3	L4	L5	.	.
Fv FRAGMENT 2	H1	-1.61	0.46
	H2	0.18	2.04
	H3
	H3

	.	L1	L2	L3	L4	L5	.	.
Fv FRAGMENT 3	H1	0.92	1.59
	H2	0.69	1.31
	H3
	H3

	.	L1	L2	L3	L4	L5	.	.
Fv FRAGMENT 4	H1

FIG.10

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RESIDUE PAIRS		AVERAGE	Strd.DEV.	MAX	MIN	MEDIAN
H1	L1	-0.72	1.42	0.92	-1.61	-1.47
H1	L2	0.68	0.82	1.59	-0.01	0.46
H1	L3
H1	L4
.
H1	L106
H2	L1	0.45	0.26	0.69	0.18	0.48
H2	L2	0.68	0.82	1.59	-0.01	0.46
H2	L3
H2	L4
.
H2	L106
H3	L1

FIG.11A

DRAFT 10/25/1990

RESIDUE PAIRS		AVERAGE	Strd.DEV.	MAX	MIN	MEDIAN
H1	L1	-0.68	1.04	0.92	-2.20	0.83
H1	L2	0.34	0.82	2.37	-0.54	0.09
H1	L3
H1	L4
.
H1	L106
H2	L1	0.74	0.69	1.83	-0.18	0.59
H2	L2	1.78	0.50	2.55	0.75	1.94
H2	L3
H2	L4
.
H2	L106
H3	L1

FIG.11B

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Res.	AA	F	AA	F	AA	F	AA	F	AA	F	AA	F
1	Glu	58	Glu	24	Asp	3	Glu	3	Gly	2	Ala	1
2	Val	99	Ile	2	Ala	1	Glu	1	Met	1	-	-
3	Gln	90	Thr	5	Glu	3	His	2	Leu	2	Lys	2
4	Leu	101	Val	3	-	-	-	-	-	-	-	-

FIG.12A

Amino Acid	van der Waals volumes [A ³]	Hydrophobicity
Ala	67	0.62
Arg	148	-2.50
Asn	96	-0.78
Asp	91	-0.90
Cys	86	0.29
Gln	114	-0.85
Glu	109	-0.79
Gly	48	0.30
His	118	-0.40
Ile	124	1.40
Leu	124	1.10
Lys	135	-1.50
Met	124	0.64
Phe	135	1.20
Pro	90	0.12
Ser	73	-0.18
Thr	93	-0.05
Trp	163	0.81
Tyr	141	0.26
Val	105	1.10

FIG.12B

Res.	AA	F	AA	F	AA	F	AA	F	AA	F	AA	F
1	109	61	109	24	91	3	48	2	67	1	-	-
2	105	99	124	2	67	1	109	1	124	1	-	-
3	114	90	93	5	109	3	118	2	124	2	135	2
4	124	101	105	3	-	-	-	-	-	-	-	-

FIG.12C

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TUTORIAL SERIES 40

VAN DER WAALS VOLUMES

CHAIN	K&W	CONS.	WEIGHTED AVERAGE	WEIGHTED StDev.	UNWEIGHTED AVERAGE	UNWEIGHTED StDev.
H	1	Glu	108	11	90	27
H	2	Val	105	5	106	23
H	3	Gln	114	6	116	14
H	4	Leu	123	3	115	13

FIG. 13A

HYDROPHOBICITY

CHAIN	K&W	CONS.	WEIGHTED AVERAGE	WEIGHTED StDev.	UNWEIGHTED AVERAGE	UNWEIGHTED StDev.
H	1	Glu	-0.77	0.24	-0.37	0.72
H	2	Val	1.08	0.20	0.59	0.84
H	3	Gln	-0.78	0.33	-0.42	0.89
H	4	Leu	1.10	0.00	1.10	0.00

FIG. 13B

TUTORIAL SECTION

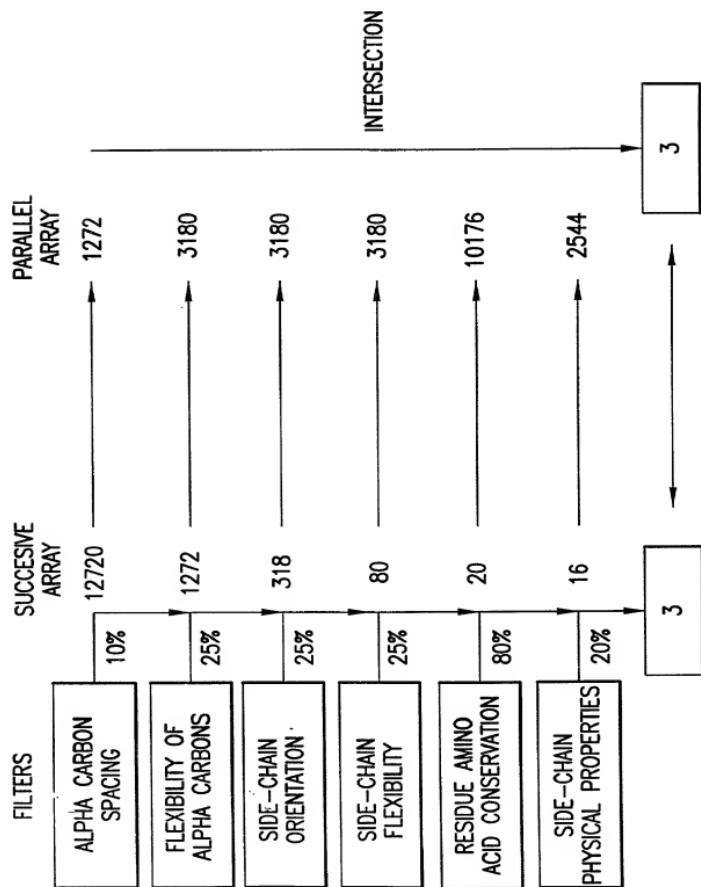


FIG. 14

C. Antarctica Lipase B Nucleotide and Amino Acid Sequence

10	20	30	40	50	60
ctaccccccgggttcggacccctgcctttcgacggccaaactcggtgctcgatgcgggtctg					
L P S G S D P A F S Q P K S V L D A G L					
70 80 90 100 110 120					
acctggccagggtgttcggacccctgcgttccaaaccatccttcgtccggaaacc					
T C Q G A S P S S V S K P I L L V P G T					
130 140 150 160 170 180					
ggcacacagggtccacagtgttcggactcgaaactggatccccctcaacgcagggt					
G T T G P Q S F D S N W I P L S T T Q L G					
190 200 210 220 230 240					
tacacaccctgtggatctaccccccgggtcatgtcaacgcacaccaggtaacacg					
Y T P C W I S P P F M L N D T Q V N T					
250 260 270 280 290 300					
gagtagatgttcaacgcacccatcaccgcgtctacgcgtgggtcgccaaacaacag					
E Y M V N A I T A L Y A G S G N N N K L P					
310 320 330 340 350 360					
gtgttacccgtgtccagggtgggtgttcgtccacagtgggtctgaccccttcccaagt					
V L T W S Q G G L V A Q W G L T F F P S					
370 380 390 400 410 420					
atcaagggtcaacagggtcgacttatggcccttgcggcactacaaggccggcgtctc					
I R S K V D R L M A F A P D Y K G T V L					
430 440 450 460 470 480					
gcggccctctcgatcgactcgcggtaatgcacccctcgatggcagcaaaaccacgg					
A G P L D A L A V S A P S V W Q Q T T G					
490 500 510 520 530 540					
tcggcaactcaccacccgactccggaaacgcgggtgtgtacccagatcggtccaccac					
S A L T T A L R N A G G L T Q I V P T T T					
550 560 570 580 590 600					
aacctctactcgccgaccgacgagatcggtcagctcgttccaaactcgccactcgac					
N L Y S A T D E I V Q P Q V S N S P L D					
610 620 630 640 650 660					
tcatectacttcaacggaaagaacgttcaggcacaggccgtgtgtggccgtgttc					
S S Y L F N G K N V Q A Q A V C G P L F					
670 680 690 700 710 720					
gtcatcgaccatcgaggctcgctcacccgcgttccatcgatcgatcgatccgc					
V I D H A G S L T S Q F S Y V V V G R S A					
730 740 750 760 770 780					
ctgcgtccaccacccggccaggctgtcgactcgacatcgatggcattacggactcaacc					
L R S T T G Q A R S A D Y G I T D C N P					
790 800 810 820 830 840					
cttcccgccaaatgtatcgactcccgagcaaaagggtcgccggctgcgttccgtcc					
L P A N D L T P E Q K V A A A A L L A P					
850 860 870 880 890 900					
gcagctgcaggccatcgatgggggtccaaacgcagaactcgccggccgacccatgc					
A A A I V A G P K Q N C E P D L M P Y					
910 920 930 940 950					
ggccgccttgcgttaggcggaaaggactgtccggcatcgatcccccgtga					
A R P F A V G K R T C S G I V T P *					

FIG. 15A

PCR Oligos for *Candida antarctica* Lipase B**Oligos for pPal-CALB**

Primer A: 5'atg gga att cca tca tca tca tca tca cag cag cgg ect acc ttc cgg ttc gga ccc3'

Primer B: 5'ctc ttg gcg gcc gcc tat cag ggg gtg acg atg cgg g3'

Oligos for Point Mutations (made in pPal-CALB)**M1- F9Y**

primer M1F: 5'atg gga att cca tca tca tca tca tca cag cag cgg ect acc ttc cgg ttc gga ccc tgc ctA ttc gc3'

M2- W52Y

Primer M2F: 5'cga ctc gaa ctA Cat ccc cct ctc3'

Primer M2R: 5'gag agg ggg atG Tag ttc gag tcg3'

M3- F117Y

Primer M3F: 5'ggg tctg acc tAc ttc ccc agt atc3'

Primer M3R: 5'gat act ggg gaa gTa ggt cag acc c3'

Oligos for pYal-CALB**Primer C:**

5'-cgA Tga gat ttc ctt caa ttt -3'

Primer D:

5'-5'tct aga aag gtg gcg gcc gec -3'

Oligos for error-prone PCR**Primer E:**

5'gaa gct gga ttc cat cat cat c3'

Primer D:

5'-5'tct aga aag gtg gcg gcc gec -3'

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Subtilisin E Nucleotide and Amino Acid Sequence

FIG. 16A

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Subtilisin Amino Acid Alignment

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
 ALA GLN SER VAL PRO TRP GLY ILE SER ARG VAL GLN ALA PRO ALA ALA HIS ASN
 ALA GLN SER VAL PRO TYR GLY ILE SER GLN ILE LYS ALA PRO ALA LEU HIS SER
 ALA LYS CYS VAL SER TYR GLY VAL SER GLN ILE LYS ALA PRO ALA LEU HIS SER

 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36
 ARG GLY LEU THR GLY SER GLY VAL LYS VAL ALA VAL LEU ASP THR GLY ILE SER
 GLN GLY TYR THR GLY SER ASN VAL LYS VAL ALA VAL ILE ASP SER GLY ILE ASP
 GLN GLY TYR THR GLY SER ASN VAL LYS VAL ALA VAL ILE ASP SER GLY ILE ASP

 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54
 THR --- HIS PRO ASP LEU ASN ILE ARG GLY GLY ALA SER PHE VAL PRO GLY GLU
 SER SER HIS PRO ASP LEU ASN VAL ARG GLY GLY ALA SER PHE VAL PRO SER GLU
 SER SER HIS PRO ASP LEU ASN VAL ALA GLY GLY ALA SER PHE VAL PRO SER GLU

 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72
 --- --- PRO SER THR GLN ASP GLY ASN GLY HIS GLY THR HIS VAL ALA GLY THR
 THR ASN PRO TYR --- GLN ASP GLY SER SER HIS GLY GLY THR HIS VAL ALA GLY THR
 THR ASN PRO PHE --- GLN ASP ASN ASN SER HIS GLY THR HIS VAL ALA GLY THR

 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90
 ILE ALA ALA LEU ASN ASN SER ILE GLY VAL LEU GLY VAL ALA PRO ASN ALA GLU
 ILE ALA ALA LEU ASN ASN SER ILE GLY VAL LEU GLY VAL SER PRO SER ALA SER
 --- --- --- --- VAL LEU ALA VAL ALA PRO SER ALA SER

 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108
 LEU TYR ALA VAL LYS VAL LEU GLY ALA SER GLY SER GLY SER VAL SER SER ILE
 LEU TYR ALA VAL LYS VAL LEU ASN SER THR GLY SER GLY GLN TYR SER TRP ILE
 LEU TYR ALA VAL LYS VAL LEU GLY ALA ASP GLY SER GLY GLN TYR SER TRP ILE

 109 110 111 112 113 114 115 116 117 118 118 120 121 122 123 124 125 126
 ALA GLN GLY LEU GLU TRP ALA GLY ASN ASN GLY MET HIS VAL ALA ASN LEU SER
 ILE ASN GLY ILE GLU TRP ALA ILE SER ASN ASN MET ASP VAL ILE ASN MET SER
 ILE ASN GLY ILE GLU TRP ALA ILE ALA ASN ASN MET ASP VAL ILE ASN MET SER

 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144
 LEU GLY SER PRO SER PRO SER ALA THR LEU GLU GLN ALA VAL ASN SER ALA THR
 LEU GLY GLY PRO THR GLY SER THR ALA LEU LYS THR VAL VAL ASP LYS ALA VAL
 LEU GLY GLY PRO SER GLY SER ALA ALA LEU LYS ALA ALA VAL ASP LYS ALA VAL

 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162
 SER ARG GLY VAL LEU VAL VAL ALA ALA SER GLY ASN SER GLY --- ALA GLY SER
 SER SER GLY ILE VAL VAL ALA ALA ALA GLY ASN GLU GLY SER SER GLY SER
 ALA SER GLY VAL VAL VAL ALA ALA GLY ASN GLU GLY GLY THR SER GLY SER

FIG. 16B

Subtilisin Amino Acid Alignment (cont'd.)

163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
 ILE SER --- --- TYR PRO ALA ARG TYR ALA ASN ALA MET ALA VAL GLY ALA
 THR SER THR VAL GLY TYR PRO ALA LYS TYR PRO SER THR ILE ALA VAL GLY ALA
 SER SER THR VAL GLY TYR PRO GLY LYS TYR PRO SER VAL ILE ALA VAL GLY ALA

181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198
 THR ASP GLN ASN ASN ASN ARG ALA SER PHE SER GLN TYR GLY ALA GLY LEU ASP
 VAL ASN SER SER ASN GLN ARG ALA SER PHE SER SER ALA GLY SER GLU LEU ASP
 VAL ASP SER SER ASN GLN ARG ALA SER PHE SER SER VAL GLY PRO GLU LEU ASP

199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216
 ILE VAL ALA PRO GLY VAL ASN VAL GLN SER THR TYR PRO GLY SER THR TYR ALA
 VAL MET ALA PRO GLY VAL SER ILE GLN SER THR LEU PRO GLY GLY THR TYR GLY
 VAL MET ALA PRO GLY VAL SER ILE CYS SER THR LEU PRO GLY ASN LYS TYR GLY

217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234
 SER LEU ASN GLY THR SER MET ALA THR PRO HIS VAL ALA GLY ALA ALA ALA LEU
 ALA TYR ASN GLY THR CYS MET ALA THR PRO HIS VAL ALA GLY ALA ALA ALA LEU
 ALA LYS SER GLY THR SER MET ALA SER PRO HIS VAL ALA GLY ALA ALA ALA LEU

235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252
 VAL LYS GLN LYS ASN PRO SER TRP SER ASN VAL GLN ILE ARG ASN HIS LEU LYS
 ILE LEU SER LYS HIS PRO THR TRP THR ASN ALA GLN VAL ARG ASP ARG LEU GLU
 ILE LEU SER LYS HIS PRO ASN TRP THR ASN THR GLN VAL ARG SER SER LEU GLU

253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270
 ASN THR ALA THR SER LEU GLY SER THR ASN LEU TYR GLY SER GLY LEU VAL ASN
 SER THR ALA THR TYR LEU GLY ASN SER PHE TYR GLY LYS GLY LEU ILE ASN
 ASN THR THR LYS LEU GLY ASN SER PHE TYR GLY LYS GLY LEU ILE ASN

271 272 273 274 275 276
 ALA GLU ALA ALA THR ARG
 VAL GLN ALA ALA ALA GLN
 VAL GLN ALA ALA ALA GLN

- FIG. 16C

105740-5522/0050

PCR Oligos for Subtilisin E

A primer-

5'-ccg agc gttg cat atg tgg aag-3'

B-primer-

5'-tta gga tcc tta atg atg atg atg atg atg ttt tgc
agg tgc ttg tac gtt gat-3'

1- K27Y

F 5'-ggc tct aac gta **TaT** gta gct gtt atc-3'R 5'-gat aac agc tac **AtA** tac gtt aga gcc-3'

5.1- G61Y

F 5'-cca tac cag gac **TAc** agt tct cac gg-3'R 5'-cc gtg aga act **gTA** gtc ctg gta tgg-3'

2- K237Y

F 5'-tta att ctt tct **TaC** cac ccc act tgg-3'R 5'-cca agt cgg gtg **GtA** aga aag aat taa c-3'

5.2- S98Y

F 5'-aa gtg ctt gat **TAT** aca gga agc ggc-3'R 5'-gcc gct tcc tgt **ATA** atc aag cac tt-3'

3.1- D36Y

F 5'-gac agc gga att **T** aet ctt etc atc-3'R 5'-gat gag aag agt **A** aat tcc get gtc-3'

6.1- H17Y

F 5'-gcg ccg gct ctt **TaC** tct caa ggc t-3'R 5'-a gcc ttg aga **gtA** aag agc cgg cgc-3'

3.2- P210Y

F 5'-caa agc aca ctt **TAt** gga ggc act tac-3'R 5'-ta agt gcc tcc **aTA** aag tgt gct tgg-3'

6.2- P86Y

F 5'-ctg ggc gtt agc **TAT** agc gca tca tta-3'R 3'-taa tga tgc gct **ATA** gct aac gcc cag-3'

4.1- K170Y

F 5'-ggc tac cct gca **TaT** tat cct tct act a-3'R 5'-agt aga agg ata **AtA** tgc agg gta gcc-3'

7- P201Y

F 5'-gat gtg atg gct **TAt** ggc gtg tcc atc-3'R 5'-gat gga cac gcc **aTA** agc cat cac atc-3'

4.2- E195Y

F 5'-age gca ggt tct **TaT** ctt gat gtc atg -3'R 5'-cat cac atc aag **AtA** aga acc tgc gct-3'

FIG. 16D